

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Fischhoff, David A
Fuchs, Roy L
Perlak, Frederick J
- (ii) TITLE OF INVENTION: Insect Resistant Plants
- (iii) NUMBER OF SEQUENCES: 54
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arnold White and Durkee
 - (B) STREET: PO Box 4433
 - (C) CITY: Houston
 - (D) STATE: TX
 - (E) COUNTRY: USA
 - (F) ZIP: 77210-4433
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/027,998
 - (B) FILING DATE: 23-FEB-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Patterson, Melinda L
 - (B) REGISTRATION NUMBER: 33,062
 - (C) REFERENCE/DOCKET NUMBER: MOBT:195
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (713) 787-1400

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAGCGACTAT TATAATCATA CATATTTTCT ATTGGAATGA TTAAGATTCC AATAGAATAG	60
TGTATAAATT ATTTATCTTG AAAGGAGGGA TGCCTAAAA CGAAGAACAT TAAAAACATA	120
TATTTGCACC GTCTAATGGA TTTATGAAAA ATCATTTTAT CAGTTTGAAA ATTATGTATT	180
ATGATAAGAA AGGGAGGAAG AAAAATGAAT CCGAACAATC GAAGTGAACA TGATACAATA	240
AAACTACTG AAAATAATGA GGTGCCAACT AACCATGTTC AATATCCTTT AGCGGAAACT	300
CCAAATCCAA CACTAGAAGA TTTAAATTAT AAAGAGTTTT TAAGAATGAC TGCAGATAAT	360
AATACGGAAG CACTAGATAG CTCTACAACA AAAGATGTCA TTCAAAAAGG CATTTCCGTA	420
GTAGGTGATC TCCTAGGCGT AGTAGGTTTC CCGTTTGGTG GAGCGCTTGT TTCGTTTTAT	480
ACAAACTTTT TAAATACTAT TTGGCCAAGT GAAGACCCGT GGAAGGCTTT TATGGAACAA	540
GTAGAAGCAT TGATGGATCA GAAAAATAGCT GATTATGCAA AAAATAAAGC TCTTGCAGAG	600
TTACAGGGCC TTCAAAATAA TGTCGAAGAT TATGTGAGTG CATTGAGTTC ATGGCAAAAA	660
AATCCTGTGA GTTCACGAAA TCCACATAGC CAGGGGCGGA TAAGAGAGCT GTTTTCTCAA	720
GCAGAAAGTC ATTTTCGTAA TTCAATGCCT TCGTTTGCAA TTTCTGGATA CGAGGTCTA	780
TTTCTAACAA CATATGCACA AGCTGCCAAC ACACATTTAT TTTTACTAAA AGACGCTCAA	840
ATTTATGGAG AAGAATGGGG ATACGAAAAA GAAGATATTG CTGAATTTTA TAAAAGACAA	900
CTAAACTTA CGCAAGAATA TACTGACCAT TGTGTCAAAT GGTATAATGT TGGATTAGAT	960
AAATTAAGAG GTTCATCTTA TGAATCTTGG GTAAACTTTA ACCGTTATCG CAGAGAGATG	1020
ACATTAACAG TATTAGATTT AATTGCACTA TTTCCATTGT ATGATGTTTCG GCTATACCCA	1080
AAAGAAGTTA AAACCGAATT AACAAGAGAC GTTTTAACAG ATCCAATTGT CGGAGTCAAC	1140
AACCTTAGGG GCTATGGAAC AACCTTCTCT AATATAGAAA ATTATATTTCG AAAACCACAT	1200
CTATTTGACT ATCTGCATAG AATTCAATTT CACACGCGGT TCCAACCAGG ATATTATGGA	1260
AATGACTCTT TCAATTATTG GTCCGGTAAT TATGTTTCAA CTAGACCAAG CATAGGATCA	1320
AATGATATAA TCACATCTCC ATTCTATGGA AATAAATCCA GTGAACCTGT AAAAAATTTA	1380
GAATTTAATG GAGAAAAAGT CTATAGAGCC GTAGCAAATA CAAATCTTGC GGTCTGGCCG	1440
TCCGCTGTAT ATTCAGGTGT TACAAAAGTG GAATTTAGCC AATATAATGA TCAAACAGAT	1500
GAAGCAAGTA CACAAACGTA CGACTCAAAA AGAAATGTTG GCGCGGTCAG CTGGGATTCT	1560
ATCGATCAAT TGCCTCCAGA AACAACAGAT GAACCTCTAG AAAAGGGATA TAGCCATCAA	1620

CTCAATTATG TAATGTGCTT TTTAATGCAG GGTAGTAGAG GAACAATCCC AGTGTTAACT 1680
TGGACACATA AAAGTGTAGA CTTTTTTAAC ATGATTGATT CGAAAAAAT TACACAACTT 1740
CCGTTAGTAA AGGCATATAA GTTACAATCT GGTGCTTCCG TTGTCGCAGG TCCTAGGTTT 1800
ACAGGAGGAG ATATCATTCA ATGCACAGAA AATGGAAGTG CGGCAACTAT TTACGTTACA 1860
CCGGATGTGT CGTACTCTCA AAAATATCGA GCTAGAATTC ATTATGCTTC TACATCTCAG 1920
ATAACATTTA CACTCAGTTT AGACGGGGCA CCATTTAATC AATACTATTT CGATAAAACG 1980
ATAAATAAAG GAGACACATT AACGTATAAT TCATTTAATT TAGCAAGTTT CAGCACACCA 2040
TTCGAATTAT CAGGGAATAA CTTACAAATA GCGTCACAG GATTAAGTGC TGGAGATAAA 2100
GTTTATATAG ACAAATGA ATTTATTCCA GTGAATTAAA TTAAGTAGAA AGTAAAGAAG 2160
TAGTGACCAT CTATGATAGT AAGCAAAGGA TAAAAAATG AGTTCATAAA ATGAATAACA 2220
TAGTGTTCTT CAACTTTCGC TTTTGAAGG TAGATGAAGA AACTATTTT TATTTTCAAA 2280
ATGAAGGAAG TTTTAAATAT GTAATCATTT AAAGGGAACA ATGAAAGTAG GAAATAAGTC 2340
ATTATCTATA ACAAATAAC CATTTTATA TAGCCAGAAA TGAATTATAA TATTAATCTT 2400
TTCTAAATTG ACGTTTTTCT AAACGTTCTA TAGCTTCAAG ACGCTTAGAA TCATCAATAT 2460
TTGTATACAG AGCTGTTGTT TCCATCGAGT TATGTCCCAT TTGATTCGCT AATAGAACAA 2520
GATCTTTATT TTCGTTATAA TGATTGGTTG CATAAGTATG GCGTAATTTA TGAGGGCTTT 2580
TCTTTTCATC CAAAAGCCAA GTGTATTTCT CTGTA 2615

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile	Lys	Thr	Thr	Glu
1				5					10					15	
Asn	Asn	Glu	Val	Pro	Thr	Asn	His	Val	Gln	Tyr	Pro	Leu	Ala	Glu	Thr
			20					25						30	

Pro Asn Pro Thr Leu Glu Asp Leu Asn Tyr Lys Glu Phe Leu Arg Met
 35 40 45
 Thr Ala Asp Asn Asn Thr Glu Ala Leu Asp Ser Ser Thr Thr Lys Asp
 50 55 60
 Val Ile Gln Lys Gly Ile Ser Val Val Gly Asp Leu Leu Gly Val Val
 65 70 75 80
 Gly Phe Pro Phe Gly Gly Ala Leu Val Ser Phe Tyr Thr Asn Phe Leu
 85 90 95
 Asn Thr Ile Trp Pro Ser Glu Asp Pro Trp Lys Ala Phe Met Glu Gln
 100 105 110
 Val Glu Ala Leu Met Asp Gln Lys Ile Ala Asp Tyr Ala Lys Asn Lys
 115 120 125
 Ala Leu Ala Glu Leu Gln Gly Leu Gln Asn Asn Val Glu Asp Tyr Val
 130 135 140
 Ser Ala Leu Ser Ser Trp Gln Lys Asn Pro Val Ser Ser Arg Asn Pro
 145 150 155 160
 His Ser Gln Gly Arg Ile Arg Glu Leu Phe Ser Gln Ala Glu Ser His
 165 170 175
 Phe Arg Asn Ser Met Pro Ser Phe Ala Ile Ser Gly Tyr Glu Val Leu
 180 185 190
 Phe Leu Thr Thr Tyr Ala Gln Ala Ala Asn Thr His Leu Phe Leu Leu
 195 200 205
 Lys Asp Ala Gln Ile Tyr Gly Glu Glu Trp Gly Tyr Glu Lys Glu Asp
 210 215 220
 Ile Ala Glu Phe Tyr Lys Arg Gln Leu Lys Leu Thr Gln Glu Tyr Thr
 225 230 235 240
 Asp His Cys Val Lys Trp Tyr Asn Val Gly Leu Asp Lys Leu Arg Gly
 245 250 255
 Ser Ser Tyr Glu Ser Trp Val Asn Phe Asn Arg Tyr Arg Arg Glu Met
 260 265 270
 Thr Leu Thr Val Leu Asp Leu Ile Ala Leu Phe Pro Leu Tyr Asp Val
 275 280 285
 Arg Leu Tyr Pro Lys Glu Val Lys Thr Glu Leu Thr Arg Asp Val Leu
 290 295 300
 Thr Asp Pro Ile Val Gly Val Asn Asn Leu Arg Gly Tyr Gly Thr Thr
 305 310 315 320

Phe	Ser	Asn	Ile	Glu	Asn	Tyr	Ile	Arg	Lys	Pro	His	Leu	Phe	Asp	Tyr	325	330	335
Leu	His	Arg	Ile	Gln	Phe	His	Thr	Arg	Phe	Gln	Pro	Gly	Tyr	Tyr	Gly	340	345	350
Asn	Asp	Ser	Phe	Asn	Tyr	Trp	Ser	Gly	Asn	Tyr	Val	Ser	Thr	Arg	Pro	355	360	365
Ser	Ile	Gly	Ser	Asn	Asp	Ile	Ile	Thr	Ser	Pro	Phe	Tyr	Gly	Asn	Lys	370	375	380
Ser	Ser	Glu	Pro	Val	Gln	Asn	Leu	Glu	Phe	Asn	Gly	Glu	Lys	Val	Tyr	385	390	395
Arg	Ala	Val	Ala	Asn	Thr	Asn	Leu	Ala	Val	Trp	Pro	Ser	Ala	Val	Tyr	405	410	415
Ser	Gly	Val	Thr	Lys	Val	Glu	Phe	Ser	Gln	Tyr	Asn	Asp	Gln	Thr	Asp	420	425	430
Glu	Ala	Ser	Thr	Gln	Thr	Tyr	Asp	Ser	Lys	Arg	Asn	Val	Gly	Ala	Val	435	440	445
Ser	Trp	Asp	Ser	Ile	Asp	Gln	Leu	Pro	Pro	Glu	Thr	Thr	Asp	Glu	Pro	450	455	460
Leu	Glu	Lys	Gly	Tyr	Ser	His	Gln	Leu	Asn	Tyr	Val	Met	Cys	Phe	Leu	465	470	475
Met	Gln	Gly	Ser	Arg	Gly	Thr	Ile	Pro	Val	Leu	Thr	Trp	Thr	His	Lys	485	490	495
Ser	Val	Asp	Phe	Phe	Asn	Met	Ile	Asp	Ser	Lys	Lys	Ile	Thr	Gln	Leu	500	505	510
Pro	Leu	Val	Lys	Ala	Tyr	Lys	Leu	Gln	Ser	Gly	Ala	Ser	Val	Val	Ala	515	520	525
Gly	Pro	Arg	Phe	Thr	Gly	Gly	Asp	Ile	Ile	Gln	Cys	Thr	Glu	Asn	Gly	530	535	540
Ser	Ala	Ala	Thr	Ile	Tyr	Val	Thr	Pro	Asp	Val	Ser	Tyr	Ser	Gln	Lys	545	550	555
Tyr	Arg	Ala	Arg	Ile	His	Tyr	Ala	Ser	Thr	Ser	Gln	Ile	Thr	Phe	Thr	565	570	575
Leu	Ser	Leu	Asp	Gly	Ala	Pro	Phe	Asn	Gln	Tyr	Tyr	Phe	Asp	Lys	Thr	580	585	590
Ile	Asn	Lys	Gly	Asp	Thr	Leu	Thr	Tyr	Asn	Ser	Phe	Asn	Leu	Ala	Ser	595	600	605

Phe Ser Thr Pro Phe Glu Leu Ser Gly Asn Asn Leu Gln Ile Gly Val
 610 615 620

Thr Gly Leu Ser Ala Gly Asp Lys Val Tyr Ile Asp Lys Ile Glu Phe
 625 630 635 640

Ile Pro Val Asn

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asn Pro Asn Asn Arg Ser Glu His Asp Thr Ile Lys Thr Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGAATCCNA ATAATCGNTC NGAACATGAT ACNATTAAAA CNACN

45

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGAACCCNA ACAACAGAAG TGAGCACGAC ACNATCAAGA CNACN

45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGAATCCNA ATAATCGGTC CGAACATGAT ACNATAAAAA CNACN

45

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAAYCCNA AYAAAYCG

17

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GARCAYGAYA CRATHAA

17

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAACAATCC CAGTGTTTAG TAGGTAGCTA GCCAGATCTT TATTT

45

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAATAAAGAT CTGGCTAGCT ACCTACTAAA CACTGGGATT GTTCC

45

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly	Thr	Ile	Pro	Val	Phe	Ser	Arg	Leu	Ala	Arg	Ser	Leu	Phe
1					5					10			

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTACAGGCGG AGATTAGTAG GTAGCTAGCC AGATCTTTAT TTTC

44

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAAAATAAAG ATCTGGCTAG CTACCTACTA ATCTCCGCCT GTAA

44

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Thr	Gly	Gly	Asp	Val	Ala	Ser	Gln	Ile	Phe	Ile	Phe
1				5					10		

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTCAGTTT TAG ACGGGGCTAG TAGGTAGCTA GCCAGATCTT TATTT

45

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAATAAAGAT CTGGCTAGCT ACCTACTAGC CCCGTCTAAA CTGAG

45

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu	Ser	Leu	Asp	Gly	Ala	Ser	Arg	Leu	Ala	Arg	Ser	Leu	Phe
1				5				10					

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTTTATATAG ACAAAAATTGA ATTTAGTAGG TAGCTAGCCA GATCTTTATT TT

52

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAAATAAAGA TCTGGCTAGC TACCTACTAA ATTCAATTTT GTCTATATAA AC

52

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Val	Tyr	Ile	Asp	Lys	Ile	Glu	Phe	Ser	Arg	Leu	Ala	Arg	Ser	Leu	Phe
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TATAAAGAGT TTTTAAGAAT AACTGCAGAT AATAATA

37

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TATTATTATC TGCAGTTATT CTAAAAAACT CTTTATA

37

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr	Lys	Glu	Phe	Leu	Arg	Ile	Thr	Ala	Asp	Asn	Asn	Thr
1				5					10			

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATGGATGC AGATAATAAT ACGGAAGCAC TAGATAGCTC T

41

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGAGCTATCT AGTGCTTCCG TATTATTATC TGCATCCATG G

41

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Asp	Ala	Asp	Asn	Asn	Thr	Glu	Ala	Leu	Asp	Ser	Ser
1				5					10			

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCATGCTAGG AGTAGTAGGT TTCCCGTTTG TGGAGCGCTT G

41

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAAGCGCTCC ACAAACGGGA AACCTACTAC TCCTAGCATG G

41

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Leu	Gly	Val	Val	Gly	Phe	Pro	Phe	Val	Glu	Arg	Leu
1				5					10			

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCATGGCAAT TTGGCCAAGT GAAGAC

26

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCTTCACTT GGCCAAATTG CCATGG

26

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ala Ile Trp Pro Ser Glu Asp
1 5

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 661 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AAGCTTGCAT GCCTGCAGGT CCGATGTGAG ACTTTTCAAC AAAGGGTAAT ATCCGGAAAC	60
CTCCTCGGAT TCCATTGCCC AGCTATCTGT CACTTTATTG TGAAGATAGT GGAAAAGGAA	120
GGTGGCTCCT ACAAATGCCA TCATTGCGAT AAAGGAAAAG CCATCGTTGA AGATGCCTCT	180
GCCGACAGTG GTCCCAAAGA TGGACCCCCA CCCACGAGGA GCATCGTGGA AAAAGAAGAC	240
GTTCCAACCA CGTCTTCAAA GCAAGTGGAT TGATGTGATG GTCCGATGTG AGACTTTTCA	300
ACAAAGGGTA ATATCCGGAA ACCTCCTCGG ATTCCATTGC CCAGCTATCT GTCACCTTAT	360
TGTGAAGATA GTGGAAAAGG AAGGTGGCTC CTACAAATGC CATCATTGCG ATAAAGGAAA	420
GGCCATCGTT GAAGATGCCT CTGCCGACAG TGGTCCCAAA GATGGACCCC CACCCACGAG	480
GAGCATCGTG GAAAAAGAAG ACGTTCCAAC CACGTCTTCA AAGCAAGTGG ATTGATGTGA	540
TATCTCCACT GACGTAAGGG ATGACGCACA ATCCCACTAT CCTTCGCAAG ACCCTTCCTC	600
TATATAAGGA AGTTCATTTT ATTTGGAGAG GACACGCTGA CAAGCTGACT CTAGCAGATC	660
T	661

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Xaa Pro Xaa Thr Arg Ala Leu Asp Asp Thr Ile Lys Lys Asp Val
1 5 10 15
Ile Gln Lys

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGAACATGGT TAGTTGG

17

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TAGGTGATCT CTAGGCG

17

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGAACAACCT TCTCTAATAT

20

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGAAYCCNA AYAAYCG

17

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GARCAYGAYA CYATHAA

17

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GATTGTTTCGG ATCCATGGTT CTCCTCCCT

30

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TAGTAGGTAG CTAGCCA

17

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCTGGCTA GCTACCTACT A

21

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGTATTATTA TCTGCATCCA TGGTTCTTCC TCCCT

35

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATTATTATCT GCAGTTATTC TTAAAAACTC TTTAT :

35

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TCACTTGGCC AAATTGCCAT GGTATTTAAA AAGTTTGT

38

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATGATAAGAA AGGGAGGAAG AAAAATGAAT CCGAACAAATC GAAGTGAACA TGATACAATA

60

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid

- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met	Asn	Pro	Asn	Asn	Arg	Ser	Glu	His	Asp	Thr	Ile
1			5						10		

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGGATTCATT TTAGATCTTC CTCCCTT

27

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTTTATATAG ACAAAATTGA ATTTATTCCA GTGAATTAAA TTAAGTAGAA AGTAAAGAAG

60

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Val Tyr Ile Asp Lys Ile Glu Phe Ile Pro Val Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTTCTAGTT AAAGATCTTT AATTCAGTG

29

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CCAAATCCAA CACTAGAAGA TTAAATTAT AAAGAGTTTT TAAGAATGAC TGCAGATAAT

60

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Asn Pro Thr Leu Glu Asp Leu Asn Tyr Lys Glu Phe Leu Arg Met
1 5 10 15

Thr Ala Asp Asn
 20

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATCTGCAGTC ATTGTAGATC TCTCTTTATA ATTT

34